

SEQUENCE LISTING

<110> BASF Aktiengesellschaft

<120> Method for the production of ergosta-5,7-dienol and/or its biosynthetic intermediates and/or metabolites in transgenic organisms

<130> 20020748

<160> 14

<170> PatentIn version 3.1

<210> 1

<211> 1617

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> CDS

<222> (1) .. (1617)

<223>

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gcc ttc agt atc ctg gat aca ctt aag tct atg tca tat ttg aaa ata				144
Ala Phe Ser Ile Leu Asp Thr Leu Lys Ser Met Ser Tyr Leu Lys Ile				
	35	40	45	
ttt gct act tta atc tgt att ctt ttg gtt tgg gac caa gtt gca tat				192
Phe Ala Thr Leu Ile Cys Ile Leu Leu Val Trp Asp Gln Val Ala Tyr				
	50	55	60	
caa atc aag aaa ggt tcc atc gca ggt cca aag ttt aag ttc tgg ccc				240
Gln Ile Lys Lys Gly Ser Ile Ala Gly Pro Lys Phe Lys Phe Trp Pro				
	65	70	75	80
atc atc ggt cca ttt ttg gaa tcc tta gat cca aag ttt gaa gaa tat				288
Ile Ile Gly Pro Phe Leu Glu Ser Leu Asp Pro Lys Phe Glu Glu Tyr				
	85	90	95	
aag gct aag tgg gca tcc ggt cca ctt tca tgt gtt tct att ttc cat				336
Lys Ala Lys Trp Ala Ser Gly Pro Leu Ser Cys Val Ser Ile Phe His				
	100	105	110	
aaa ttt gtt gtt atc gca tct act aga gac ttg gca aga aag atc ttg				384
Lys Phe Val Val Ile Ala Ser Thr Arg Asp Leu Ala Arg Lys Ile Leu				
	115	120	125	
caa tct tcc aaa ttc gtc aaa cct tgc gtt gtc gat gtt gct gtg aag				432
Gln Ser Ser Lys Phe Val Lys Pro Cys Val Val Asp Val Ala Val Lys				
	130	135	140	
atc tta aga cct tgc aat tgg gtt ttt ttg gac ggt aaa gct cat act				480
Ile Leu Arg Pro Cys Asn Trp Val Phe Leu Asp Gly Lys Ala His Thr				
	145	150	155	160
gat tac aga aaa tca tta aac ggt ctt ttc act aaa caa gct ttg gct				528
Asp Tyr Arg Lys Ser Leu Asn Gly Leu Phe Thr Lys Gln Ala Leu Ala				
	165	170	175	
caa tac tta cct tca ttg gaa caa atc atg gat aag tac atg gat aag				576
Gln Tyr Leu Pro Ser Leu Glu Gln Ile Met Asp Lys Tyr Met Asp Lys				
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Phe Val Arg Leu Ser Lys Glu Asn Asn Tyr Glu Pro Gln Val Phe Phe				

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cat gaa atg aga gaa att ctt tgc gcc tta tca ttg aac tct ttc tgt			672
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ggg aac tat att acc gaa gat caa gtc aga aag att gct gat gat tac			720
Gly Asn Tyr Ile Thr Glu Asp Gln Val Arg Lys Ile Ala Asp Asp Tyr			
225	230	235	240
tat ttg gtt aca gca gca ttg gaa tta gtc aac ttc cca att att atc			768
Tyr Leu Val Thr Ala Ala Leu Glu Leu Val Asn Phe Pro Ile Ile Ile			
	245	250	255
cct tac act aaa aca tgg tat ggt aag aaa act gca gac atg gcc atg			816
Pro Tyr Thr Lys Thr Trp Tyr Gly Lys Lys Thr Ala Asp Met Ala Met			
	260	265	270
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Lys Ile Phe Glu Asn Cys Ala Gln Met Ala Lys Asp His Ile Ala Ala			
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Asp Ala Lys Asn Ser Asn Asp Asp Asp Ser Arg Ile Tyr His Arg Glu			
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ttt act aac aag gaa atc tcc gaa gct gtt ttc act ttc tta ttt gct			1008
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	325	330	335
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gct gac cgt cca gat gtc tta gct aag atc aga gaa gaa caa ttg gct			1104
Ala Asp Arg Pro Asp Val Leu Ala Lys Ile Arg Glu Glu Gln Leu Ala			
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gtt cgt aac aat gac atg tct acc gaa ttg aac ttg gat ttg att gag			1152
Val Arg Asn Asn Asp Met Ser Thr Glu Leu Asn Leu Asp Leu Ile Glu			
	370	375	380
aaa atg aag tac acc aat atg gtc ata aaa gaa act ttg cgt tac aga			1200
Lys Met Lys Tyr Thr Asn Met Val Ile Lys Glu Thr Leu Arg Tyr Arg			

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Pro Pro Val Leu Met Val Pro Tyr Val Val Lys Lys Asn Phe Pro Val				
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tcc cct aac tat acc gca cca aag ggc gct atg tta att cca acc tta				1296
Ser Pro Asn Tyr Thr Ala Pro Lys Gly Ala Met Leu Ile Pro Thr Leu				
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Tyr Pro Ala Leu His Asp Pro Glu Val Tyr Glu Asn Pro Asp Glu Phe				
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aat tgg ttg gtt ttt ggt tgt ggt cca cac gtt tgc tta ggt caa aca				1440
Asn Trp Leu Val Phe Gly Cys Gly Pro His Val Cys Leu Gly Gln Thr				
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Tyr Val Met Ile Thr Phe Ala Ala Leu Leu Gly Lys Phe Ala Leu Tyr				
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Thr Asp Phe His His Thr Val Thr Pro Leu Ser Glu Lys Ile Lys Val				
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<212> PRT

<213> Saccharomyces cerevisiae

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Phe Ala Thr Leu Ile Cys Ile Leu Leu Val Trp Asp Gln Val Ala Tyr
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Gln Ile Lys Lys Gly Ser Ile Ala Gly Pro Lys Phe Lys Phe Trp Pro
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Ile Ile Gly Pro Phe Leu Glu Ser Leu Asp Pro Lys Phe Glu Glu Tyr
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Lys Ala Lys Trp Ala Ser Gly Pro Leu Ser Cys Val Ser Ile Phe His
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Lys Phe Val Val Ile Ala Ser Thr Arg Asp Leu Ala Arg Lys Ile Leu
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Gln Ser Ser Lys Phe Val Lys Pro Cys Val Val Asp Val Ala Val Lys
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Asp Tyr Arg Lys Ser Leu Asn Gly Leu Phe Thr Lys Gln Ala Leu Ala
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6

Gln Tyr Leu Pro Ser Leu Glu Gln Ile Met Asp Lys Tyr Met Asp Lys
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Phe Val Arg Leu Ser Lys Glu Asn Asn Tyr Glu Pro Gln Val Phe Phe
195 200 205

His Glu Met Arg Glu Ile Leu Cys Ala Leu Ser Leu Asn Ser Phe Cys
210 215 220

Gly Asn Tyr Ile Thr Glu Asp Gln Val Arg Lys Ile Ala Asp Asp Tyr
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Tyr Leu Val Thr Ala Ala Leu Glu Leu Val Asn Phe Pro Ile Ile Ile
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Pro Tyr Thr Lys Thr Trp Tyr Gly Lys Lys Thr Ala Asp Met Ala Met
260 265 270

Lys Ile Phe Glu Asn Cys Ala Gln Met Ala Lys Asp His Ile Ala Ala
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Gly Gly Lys Pro Val Cys Val Met Asp Ala Trp Cys Lys Leu Met His
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Asp Ala Lys Asn Ser Asn Asp Asp Asp Ser Arg Ile Tyr His Arg Glu
305 310 315 320

Phe Thr Asn Lys Glu Ile Ser Glu Ala Val Phe Thr Phe Leu Phe Ala
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Ser Gln Asp Ala Ser Ser Ser Leu Ala Cys Trp Leu Phe Gln Ile Val
340 345 350

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355 360 365

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370 375 380

Lys Met Lys Tyr Thr Asn Met Val Ile Lys Glu Thr Leu Arg Tyr Arg
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Pro Pro Val Leu Met Val Pro Tyr Val Val Lys Lys Asn Phe Pro Val
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Ser Pro Asn Tyr Thr Ala Pro Lys Gly Ala Met Leu Ile Pro Thr Leu
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Tyr Pro Ala Leu His Asp Pro Glu Val Tyr Glu Asn Pro Asp Glu Phe
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485 490 495

Thr Asp Phe His His Thr Val Thr Pro Leu Ser Glu Lys Ile Lys Val
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<213> Artificial sequence

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tct gga tcg aaa gtc aaa agt tta tca tct gcg caa tcg agc tca tca	144
Ser Gly Ser Lys Val Lys Ser Leu Ser Ser Ala Gln Ser Ser Ser Ser	
35 40 45	

gga cct tca tca tct agt gag gaa gat gat tcc cgc gat att gaa agc	192
Gly Pro Ser Ser Ser Ser Glu Glu Asp Asp Ser Arg Asp Ile Glu Ser	
50 55 60	

ttg gat aag aaa ata cgt cct tta gaa gaa tta gaa gca tta tta agt	240
Leu Asp Lys Lys Ile Arg Pro Leu Glu Glu Leu Glu Ala Leu Leu Ser	
65 70 75 80	

agt gga aat aca aaa caa ttg aag aac aaa gag gtc gct gcc ttg gtt	288
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85 90 95	

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Ile His Gly Lys Leu Pro Leu Tyr Ala Leu Glu Lys Lys Leu Gly Asp	
100 105 110	

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115 120 125	

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Glu Ala Pro Val Leu Ala Ser Asp Arg Leu Pro Tyr Lys Asn Tyr Asp	
130 135 140	
tac gac cgc gta ttt ggc gct tgt tgt gaa aat gtt ata ggt tac atg	480
Tyr Asp Arg Val Phe Gly Ala Cys Cys Glu Asn Val Ile Gly Tyr Met	
145 150 155 160	
cct ttg ccc gtt ggt gtt ata ggc ccc ttg gtt atc gat ggt aca tct	528
Pro Leu Pro Val Gly Val Ile Gly Pro Leu Val Ile Asp Gly Thr Ser	
165 170 175	
tat cat ata cca atg gca act aca gag ggt tgt ttg gta gct tct gcc	576
Tyr His Ile Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala Ser Ala	
180 185 190	
atg cgt ggc tgt aag gca atc aat gct ggc ggt ggt gca aca act gtt	624
Met Arg Gly Cys Lys Ala Ile Asn Ala Gly Gly Gly Ala Thr Thr Val	
195 200 205	
tta act aag gat ggt atg aca aga ggc cca gta gtc cgt ttc cca act	672
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caa aac gca att aaa aaa gct ttt aac tct aca tca aga ttt gca cgt	768
Gln Asn Ala Ile Lys Lys Ala Phe Asn Ser Thr Ser Arg Phe Ala Arg	
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260 265 270	
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Phe Arg Thr Thr Thr Gly Asp Ala Met Gly Met Asn Met Ile Ser Lys	
275 280 285	
ggg gtc gaa tac tca tta aag caa atg gta gaa gag tat ggc tgg gaa	912
Gly Val Glu Tyr Ser Leu Lys Gln Met Val Glu Glu Tyr Gly Trp Glu	
290 295 300	
gat atg gag gtt gtc tcc gtt tct ggt aac tac tgt acc gac aaa aaa	960
Asp Met Glu Val Val Ser Val Ser Gly Asn Tyr Cys Thr Asp Lys Lys	
305 310 315 320	

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Arg Ile Ser Val Ser Met Pro Ser Ile Glu Val Gly Thr Ile Gly Gly	
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ggg act gtt cta gaa cca caa ggt gcc atg ttg gac tta tta ggt gta	1344
Gly Thr Val Leu Glu Pro Gln Gly Ala Met Leu Asp Leu Leu Gly Val	
435 440 445	
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Arg Gly Pro His Ala Thr Ala Pro Gly Thr Asn Ala Arg Gln Leu Ala	
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Arg Ile Val Ala Cys Ala Val Leu Ala Gly Glu Leu Ser Leu Cys Ala	
465 470 475 480	
gcc cta gca gcc ggc cat ttg gtt caa agt cat atg acc cac aac agg	1488
Ala Leu Ala Ala Gly His Leu Val Gln Ser His Met Thr His Asn Arg	
485 490 495	
aaa cct gct gaa cca aca aaa cct aac aat ttg gac gcc act gat ata	1536
Lys Pro Ala Glu Pro Thr Lys Pro Asn Asn Leu Asp Ala Thr Asp Ile	
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<212> PRT

<213> Artificial sequence

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Ser Gly Ser Lys Val Lys Ser Leu Ser Ser Ala Gln Ser Ser Ser Ser
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Gly Pro Ser Ser Ser Ser Glu Glu Asp Asp Ser Arg Asp Ile Glu Ser
50 55 60

Leu Asp Lys Lys Ile Arg Pro Leu Glu Glu Leu Glu Ala Leu Leu Ser
65 70 75 80

Ser Gly Asn Thr Lys Gln Leu Lys Asn Lys Glu Val Ala Ala Leu Val
85 90 95

Ile His Gly Lys Leu Pro Leu Tyr Ala Leu Glu Lys Lys Leu Gly Asp
100 105 110

Thr Thr Arg Ala Val Ala Val Arg Arg Lys Ala Leu Ser Ile Leu Ala
115 120 125

12

Glu Ala Pro Val Leu Ala Ser Asp Arg Leu Pro Tyr Lys Asn Tyr Asp
 130 135 140

Tyr Asp Arg Val Phe Gly Ala Cys Cys Glu Asn Val Ile Gly Tyr Met
 145 150 155 160

Pro Leu Pro Val Gly Val Ile Gly Pro Leu Val Ile Asp Gly Thr Ser
 165 170 175

Tyr His Ile Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala Ser Ala
 180 185 190

Met Arg Gly Cys Lys Ala Ile Asn Ala Gly Gly Gly Ala Thr Thr Val
 195 200 205

Leu Thr Lys Asp Gly Met Thr Arg Gly Pro Val Val Arg Phe Pro Thr
 210 215 220

Leu Lys Arg Ser Gly Ala Cys Lys Ile Trp Leu Asp Ser Glu Glu Gly
 225 230 235 240

Gln Asn Ala Ile Lys Lys Ala Phe Asn Ser Thr Ser Arg Phe Ala Arg
 245 250 255

Leu Gln His Ile Gln Thr Cys Leu Ala Gly Asp Leu Leu Phe Met Arg
 260 265 270

Phe Arg Thr Thr Thr Gly Asp Ala Met Gly Met Asn Met Ile Ser Lys
 275 280 285

Gly Val Glu Tyr Ser Leu Lys Gln Met Val Glu Glu Tyr Gly Trp Glu
 290 295 300

Asp Met Glu Val Val Ser Val Ser Gly Asn Tyr Cys Thr Asp Lys Lys
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13

Pro Ala Ala Ile Asn Trp Ile Glu Gly Arg Gly Lys Ser Val Val Ala
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Glu Ala Thr Ile Pro Gly Asp Val Val Arg Lys Val Leu Lys Ser Asp
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Val Ser Ala Leu Val Glu Leu Asn Ile Ala Lys Asn Leu Val Gly Ser
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Ala Met Ala Gly Ser Val Gly Gly Phe Asn Ala His Ala Ala Asn Leu
370 375 380

Val Thr Ala Val Phe Leu Ala Leu Gly Gln Asp Pro Ala Gln Asn Val
385 390 395 400

Glu Ser Ser Asn Cys Ile Thr Leu Met Lys Glu Val Asp Gly Asp Leu
405 410 415

Arg Ile Ser Val Ser Met Pro Ser Ile Glu Val Gly Thr Ile Gly Gly
420 425 430

Gly Thr Val Leu Glu Pro Gln Gly Ala Met Leu Asp Leu Leu Gly Val
435 440 445

Arg Gly Pro His Ala Thr Ala Pro Gly Thr Asn Ala Arg Gln Leu Ala
450 455 460

Arg Ile Val Ala Cys Ala Val Leu Ala Gly Glu Leu Ser Leu Cys Ala
465 470 475 480

Ala Leu Ala Ala Gly His Leu Val Gln Ser His Met Thr His Asn Arg
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<212> DNA

<213> Saccharomyces cerevisiae

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<221> CDS

<222> (1) .. (1593)

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Phe Asn Ala Lys Leu Ala Asp Val Ser Ala Glu Ala Tyr Ala His	
115 120 125	
ttg act act cca gtt ttc ggt aaa ggt gtt att tac gat tgt cca aat	432
Leu Thr Thr Pro Val Phe Gly Lys Gly Val Ile Tyr Asp Cys Pro Asn	
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tct aga ttg atg gag caa aag aag ttt gtt aag ggt gct cta acc aaa	480
Ser Arg Leu Met Glu Gln Lys Lys Phe Val Lys Gly Ala Leu Thr Lys	
145 150 155 160	
gaa gcc ttc aag agc tac gtt cca ttg att gct gaa gaa gtg tac aag	528
Glu Ala Phe Lys Ser Tyr Val Pro Leu Ile Ala Glu Glu Val Tyr Lys	
165 170 175	
tac ttc aga gac tcc aaa aac ttc cgt ttg aat gaa aga act act ggt	576
Tyr Phe Arg Asp Ser Lys Asn Phe Arg Leu Asn Glu Arg Thr Thr Gly	
180 185 190	
act att gac gtg atg gtt act caa cct gaa atg act att ttc acc gct	624
Thr Ile Asp Val Met Val Thr Gln Pro Glu Met Thr Ile Phe Thr Ala	
195 200 205	
tca aga tca tta ttg ggt aag gaa atg aga gca aaa ttg gat acc gat	672
Ser Arg Ser Leu Leu Gly Lys Glu Met Arg Ala Lys Leu Asp Thr Asp	
210 215 220	
ttt gct tac ttg tac agt gat ttg gat aag ggt ttc act cca atc aac	720
Phe Ala Tyr Leu Tyr Ser Asp Leu Asp Lys Gly Phe Thr Pro Ile Asn	
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ttc gtc ttc cct aac tta cca ttg gaa cac tat aga aag aga gat cac	768
Phe Val Phe Pro Asn Leu Pro Leu Glu His Tyr Arg Lys Arg Asp His	
245 250 255	
gct caa aag gct atc tcc ggt act tac atg tct ttg att aag gaa aga	816
Ala Gln Lys Ala Ile Ser Gly Thr Tyr Met Ser Leu Ile Lys Glu Arg	
260 265 270	
aga aag aac aac gac att caa gac aga gat ttg atc gat tcc ttg atg	864
Arg Lys Asn Asn Asp Ile Gln Asp Arg Asp Leu Ile Asp Ser Leu Met	
275 280 285	

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290 295 300	
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Ala Asn Leu Leu Ile Gly Val Leu Met Gly Gly Gln His Thr Ser Ala	
305 310 315 320	
 gcc act tct gct tgg att ttg ttg cac ttg gct gaa aga cca gat gtc	1008
Ala Thr Ser Ala Trp Ile Leu Leu His Leu Ala Glu Arg Pro Asp Val	
325 330 335	
 caa caa gaa ttg tac gaa gaa caa atg cgt gtt ttg gat ggt ggt aag	1056
Gln Gln Glu Leu Tyr Glu Glu Gln Met Arg Val Leu Asp Gly Gly Lys	
340 345 350	
 aag gaa ttg acc tac gat tta tta caa gaa atg cca ttg ttg aac caa	1104
Lys Glu Leu Thr Tyr Asp Leu Leu Gln Glu Met Pro Leu Leu Asn Gln	
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 aaa gat tct gcc tcc tct tat tcc gtc ggt gaa gaa gtc gat tac ggt	1344
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 Gly Val Leu Met Ser Ile Phe Ile Arg Thr Leu Lys Trp His Tyr Pro
 485 490 495

gag ggt aag acc gtt cca cct cct gac ttt aca tct atg gtt act ctt 1536
 Glu Gly Lys Thr Val Pro Pro Pro Asp Phe Thr Ser Met Val Thr Leu
 500 505 510

cca acc ggt cca gcc aag atc atc tgg gaa aag aga aat cca gaa caa 1584
 Pro Thr Gly Pro Ala Lys Ile Ile Trp Glu Lys Arg Asn Pro Glu Gln
 515 520 525

aag atc taa 1593
 Lys Ile
 530

<210> 6

<211> 530

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 6

Met Ser Ala Thr Lys Ser Ile Val Gly Glu Ala Leu Glu Tyr Val Asn
 1 5 10 15

Ile Gly Leu Ser His Phe Leu Ala Leu Pro Leu Ala Gln Arg Ile Ser
 20 25 30

Leu Ile Ile Ile Ile Pro Phe Ile Tyr Asn Ile Val Trp Gln Leu Leu
 35 40 45

Tyr Ser Leu Arg Lys Asp Arg Pro Pro Leu Val Phe Tyr Trp Ile Pro
 50 55 60

Trp Val Gly Ser Ala Val Val Tyr Gly Met Lys Pro Tyr Glu Phe Phe
 65 70 75 80

Glu Glu Cys Gln Lys Lys Tyr Gly Asp Ile Phe Ser Phe Val Leu Leu
85 90 95

Gly Arg Val Met Thr Val Tyr Leu Gly Pro Lys Gly His Glu Phe Val
100 105 110

Phe Asn Ala Lys Leu Ala Asp Val Ser Ala Glu Ala Ala Tyr Ala His
115 120 125

Leu Thr Thr Pro Val Phe Gly Lys Gly Val Ile Tyr Asp Cys Pro Asn
130 135 140

Ser Arg Leu Met Glu Gln Lys Lys Phe Val Lys Gly Ala Leu Thr Lys
145 150 155 160

Glu Ala Phe Lys Ser Tyr Val Pro Leu Ile Ala Glu Glu Val Tyr Lys
165 170 175

Tyr Phe Arg Asp Ser Lys Asn Phe Arg Leu Asn Glu Arg Thr Thr Gly
180 185 190

Thr Ile Asp Val Met Val Thr Gln Pro Glu Met Thr Ile Phe Thr Ala
195 200 205

Ser Arg Ser Leu Leu Gly Lys Glu Met Arg Ala Lys Leu Asp Thr Asp
210 215 220

Phe Ala Tyr Leu Tyr Ser Asp Leu Asp Lys Gly Phe Thr Pro Ile Asn
225 230 235 240

Phe Val Phe Pro Asn Leu Pro Leu Glu His Tyr Arg Lys Arg Asp His
245 250 255

Ala Gln Lys Ala Ile Ser Gly Thr Tyr Met Ser Leu Ile Lys Glu Arg
260 265 270

Arg Lys Asn Asn Asp Ile Gln Asp Arg Asp Leu Ile Asp Ser Leu Met
 275 280 285

Lys Asn Ser Thr Tyr Lys Asp Gly Val Lys Met Thr Asp Gln Glu Ile
 290 295 300

Ala Asn Leu Leu Ile Gly Val Leu Met Gly Gly Gln His Thr Ser Ala
 305 310 315 320

Ala Thr Ser Ala Trp Ile Leu Leu His Leu Ala Glu Arg Pro Asp Val
 325 330 335

Gln Gln Glu Leu Tyr Glu Glu Gln Met Arg Val Leu Asp Gly Gly Lys
 340 345 350

Lys Glu Leu Thr Tyr Asp Leu Leu Gln Glu Met Pro Leu Leu Asn Gln
 355 360 365

Thr Ile Lys Glu Thr Leu Arg Met His His Pro Leu His Ser Leu Phe
 370 375 380

Arg Lys Val Met Lys Asp Met His Val Pro Asn Thr Ser Tyr Val Ile
 385 390 395 400

Pro Ala Gly Tyr His Val Leu Val Ser Pro Gly Tyr Thr His Leu Arg
 405 410 415

Asp Glu Tyr Phe Pro Asn Ala His Gln Phe Asn Ile His Arg Trp Asn
 420 425 430

Lys Asp Ser Ala Ser Ser Tyr Ser Val Gly Glu Glu Val Asp Tyr Gly
 435 440 445

Phe Gly Ala Ile Ser Lys Gly Val Ser Ser Pro Tyr Leu Pro Phe Gly
 450 455 460

Gly Gly Arg His Arg Cys Ile Gly Glu His Phe Ala Tyr Cys Gln Leu
 465 470 475 480

Gly Val Leu Met Ser Ile Phe Ile Arg Thr Leu Lys Trp His Tyr Pro
 485 490 495

Glu Gly Lys Thr Val Pro Pro Pro Asp Phe Thr Ser Met Val Thr Leu
 500 505 510

Pro Thr Gly Pro Ala Lys Ile Ile Trp Glu Lys Arg Asn Pro Glu Gln
 515 520 525

Lys Ile
 530

<210> 7

<211> 1491

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1491)

<223>

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 Met Ser Ala Val Asn Val Ala Pro Glu Leu Ile Asn Ala Asp Asn Thr
 1 5 10 15

att acc tac gat gcg att gtc atc ggt gct ggt gtt atc ggt cca tgt 96

21

Ile Thr Tyr Asp Ala Ile Val Ile Gly Ala Gly Val Ile Gly Pro Cys	
20 25 30	
ggt gct act ggt cta gca aga aag ggt aag aaa gtt ctt atc gta gaa	144
Val Ala Thr Gly Leu Ala Arg Lys Gly Lys Lys Val Leu Ile Val Glu	
35 40 45	
cgt gac tgg gct atg cct gat aga att gtt ggt gaa ttg atg caa cca	192
Arg Asp Trp Ala Met Pro Asp Arg Ile Val Gly Glu Leu Met Gln Pro	
50 55 60	
ggt ggt gtt aga gca ttg aga agt ctg ggt atg att caa tct atc aac	240
Gly Gly Val Arg Ala Leu Arg Ser Leu Gly Met Ile Gln Ser Ile Asn	
65 70 75 80	
aac atc gaa gca tat cct gtt acc ggt tat acc gtc ttt ttc aac ggc	288
Asn Ile Glu Ala Tyr Pro Val Thr Gly Tyr Thr Val Phe Phe Asn Gly	
85 90 95	
gaa caa gtt gat att cca tac cct tac aag gcc gat atc cct aaa gtt	336
Glu Gln Val Asp Ile Pro Tyr Pro Tyr Lys Ala Asp Ile Pro Lys Val	
100 105 110	
gaa aaa ttg aag gac ttg gtc aaa gat ggt aat gac aag gtc ttg gaa	384
Glu Lys Leu Lys Asp Leu Val Lys Asp Gly Asn Asp Lys Val Leu Glu	
115 120 125	
gac agc act att cac atc aag gat tac gaa gat gat gaa aga gaa agg	432
Asp Ser Thr Ile His Ile Lys Asp Tyr Glu Asp Asp Glu Arg Glu Arg	
130 135 140	
ggt gtt gct ttt gtt cat ggt aga ttc ttg aac aac ttg aga aac att	480
Gly Val Ala Phe Val His Gly Arg Phe Leu Asn Asn Leu Arg Asn Ile	
145 150 155 160	
act gct caa gag cca aat gtt act aga gtg caa ggt aac tgt att gag	528
Thr Ala Gln Glu Pro Asn Val Thr Arg Val Gln Gly Asn Cys Ile Glu	
165 170 175	
ata ttg aag gat gaa aag aat gag gtt gtt ggt gcc aag gtt gac att	576
Ile Leu Lys Asp Glu Lys Asn Glu Val Val Gly Ala Lys Val Asp Ile	
180 185 190	
gat ggc cgt ggc aag gtg gaa ttc aaa gcc cac ttg aca ttt atc tgt	624
Asp Gly Arg Gly Lys Val Glu Phe Lys Ala His Leu Thr Phe Ile Cys	
195 200 205	
gac ggt atc ttt tca cgt ttc aga aag gaa ttg cac cca gac cat gtt	672

22

Asp Gly Ile Phe Ser Arg Phe Arg Lys Glu Leu His Pro Asp His Val	
210 215 220	
cca act gtc ggt tct tcg ttt gtc ggt atg tct ttg ttc aat gct aag	720
Pro Thr Val Gly Ser Ser Phe Val Gly Met Ser Leu Phe Asn Ala Lys	
225 230 235 240	
aat cct gct cct atg cac ggt cac gtt att ctt ggt agt gat cat atg	768
Asn Pro Ala Pro Met His Gly His Val Ile Leu Gly Ser Asp His Met	
245 250 255	
cca atc ttg gtt tac caa atc agt cca gaa gaa aca aga atc ctt tgt	816
Pro Ile Leu Val Tyr Gln Ile Ser Pro Glu Glu Thr Arg Ile Leu Cys	
260 265 270	
gct tac aac tct cca aag gtc cca gct gat atc aag agt tgg atg att	864
Ala Tyr Asn Ser Pro Lys Val Pro Ala Asp Ile Lys Ser Trp Met Ile	
275 280 285	
aag gat gtc caa cct ttc att cca aag agt cta cgt cct tca ttt gat	912
Lys Asp Val Gln Pro Phe Ile Pro Lys Ser Leu Arg Pro Ser Phe Asp	
290 295 300	
gaa gcc gtc agc caa ggt aaa ttt aga gct atg cca aac tcc tac ttg	960
Glu Ala Val Ser Gln Gly Lys Phe Arg Ala Met Pro Asn Ser Tyr Leu	
305 310 315 320	
cca gct aga caa aac gac gtc act ggt atg tgt gtt atc ggt gac gct	1008
Pro Ala Arg Gln Asn Asp Val Thr Gly Met Cys Val Ile Gly Asp Ala	
325 330 335	
cta aat atg aga cat cca ttg act ggt ggt ggt atg act gtc ggt ttg	1056
Leu Asn Met Arg His Pro Leu Thr Gly Gly Gly Met Thr Val Gly Leu	
340 345 350	
cat gat gtt gtc ttg ttg att aag aaa ata ggt gac cta gac ttc agc	1104
His Asp Val Val Leu Leu Ile Lys Lys Ile Gly Asp Leu Asp Phe Ser	
355 360 365	
gac cgt gaa aag gtt ttg gat gaa tta cta gac tac cat ttc gaa aga	1152
Asp Arg Glu Lys Val Leu Asp Glu Leu Leu Asp Tyr His Phe Glu Arg	
370 375 380	
aag agt tac gat tcc gtt att aac gtt ttg tca gtg gct ttg tat tct	1200
Lys Ser Tyr Asp Ser Val Ile Asn Val Leu Ser Val Ala Leu Tyr Ser	
385 390 395 400	
ttg ttc gct gct gac agc gat aac ttg aag gca tta caa aaa ggt tgt	1248

23

Leu Phe Ala Ala Asp Ser Asp Asn Leu Lys Ala Leu Gln Lys Gly Cys
 405 410 415
 ttc aaa tat ttc caa aga ggt ggc gat tgt gtc aac aaa ccc gtt gaa 1296
 Phe Lys Tyr Phe Gln Arg Gly Gly Asp Cys Val Asn Lys Pro Val Glu
 420 425 430
 ttt ctg tct ggt gtc ttg cca aag cct ttg caa ttg acc agg gtt ttc 1344
 Phe Leu Ser Gly Val Leu Pro Lys Pro Leu Gln Leu Thr Arg Val Phe
 435 440 445
 ttc gct gtc gct ttt tac acc att tac ttg aac atg gaa gaa cgt ggt 1392
 Phe Ala Val Ala Phe Tyr Thr Ile Tyr Leu Asn Met Glu Glu Arg Gly
 450 455 460
 ttc ttg gga tta cca atg gct tta ttg gaa ggt att atg att ttg atc 1440
 Phe Leu Gly Leu Pro Met Ala Leu Leu Glu Gly Ile Met Ile Leu Ile
 465 470 475 480
 aca gct att aga gta ttc acc cca ttt ttg ttt ggt gag ttg att ggt 1488
 Thr Ala Ile Arg Val Phe Thr Pro Phe Leu Phe Gly Glu Leu Ile Gly
 485 490 495
 taa 1491

<210> 8

<211> 496

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 8

Met Ser Ala Val Asn Val Ala Pro Glu Leu Ile Asn Ala Asp Asn Thr
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Ile Thr Tyr Asp Ala Ile Val Ile Gly Ala Gly Val Ile Gly Pro Cys
 20 25 30

Val Ala Thr Gly Leu Ala Arg Lys Gly Lys Lys Val Leu Ile Val Glu
 35 40 45

Arg Asp Trp Ala Met Pro Asp Arg Ile Val Gly Glu Leu Met Gln Pro
 50 55 60

Gly Gly Val Arg Ala Leu Arg Ser Leu Gly Met Ile Gln Ser Ile Asn
 65 70 75 80

Asn Ile Glu Ala Tyr Pro Val Thr Gly Tyr Thr Val Phe Phe Asn Gly
 85 90 95

Glu Gln Val Asp Ile Pro Tyr Pro Tyr Lys Ala Asp Ile Pro Lys Val
 100 105 110

Glu Lys Leu Lys Asp Leu Val Lys Asp Gly Asn Asp Lys Val Leu Glu
 115 120 125

Asp Ser Thr Ile His Ile Lys Asp Tyr Glu Asp Asp Glu Arg Glu Arg
 130 135 140

Gly Val Ala Phe Val His Gly Arg Phe Leu Asn Asn Leu Arg Asn Ile
 145 150 155 160

Thr Ala Gln Glu Pro Asn Val Thr Arg Val Gln Gly Asn Cys Ile Glu
 165 170 175

Ile Leu Lys Asp Glu Lys Asn Glu Val Val Gly Ala Lys Val Asp Ile
 180 185 190

Asp Gly Arg Gly Lys Val Glu Phe Lys Ala His Leu Thr Phe Ile Cys
 195 200 205

Asp Gly Ile Phe Ser Arg Phe Arg Lys Glu Leu His Pro Asp His Val
 210 215 220

Pro Thr Val Gly Ser Ser Phe Val Gly Met Ser Leu Phe Asn Ala Lys
 225 230 235 240

Asn Pro Ala Pro Met His Gly His Val Ile Leu Gly Ser Asp His Met
 245 250 255

Pro Ile Leu Val Tyr Gln Ile Ser Pro Glu Glu Thr Arg Ile Leu Cys
 260 265 270

Ala Tyr Asn Ser Pro Lys Val Pro Ala Asp Ile Lys Ser Trp Met Ile
 275 280 285

Lys Asp Val Gln Pro Phe Ile Pro Lys Ser Leu Arg Pro Ser Phe Asp
 290 295 300

Glu Ala Val Ser Gln Gly Lys Phe Arg Ala Met Pro Asn Ser Tyr Leu
 305 310 315 320

Pro Ala Arg Gln Asn Asp Val Thr Gly Met Cys Val Ile Gly Asp Ala
 325 330 335

Leu Asn Met Arg His Pro Leu Thr Gly Gly Gly Met Thr Val Gly Leu
 340 345 350

His Asp Val Val Leu Leu Ile Lys Lys Ile Gly Asp Leu Asp Phe Ser
 355 360 365

Asp Arg Glu Lys Val Leu Asp Glu Leu Leu Asp Tyr His Phe Glu Arg
 370 375 380

Lys Ser Tyr Asp Ser Val Ile Asn Val Leu Ser Val Ala Leu Tyr Ser
 385 390 395 400

Leu Phe Ala Ala Asp Ser Asp Asn Leu Lys Ala Leu Gln Lys Gly Cys
 405 410 415

Phe Lys Tyr Phe Gln Arg Gly Gly Asp Cys Val Asn Lys Pro Val Glu
 420 425 430

Phe Leu Ser Gly Val Leu Pro Lys Pro Leu Gln Leu Thr Arg Val Phe
 435 440 445

Phe Ala Val Ala Phe Tyr Thr Ile Tyr Leu Asn Met Glu Glu Arg Gly
 450 455 460

Phe Leu Gly Leu Pro Met Ala Leu Leu Glu Gly Ile Met Ile Leu Ile
 465 470 475 480

Thr Ala Ile Arg Val Phe Thr Pro Phe Leu Phe Gly Glu Leu Ile Gly
 485 490 495

<210> 9

<211> 1335

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1335)

<223>

<400> 9

atg gga aag cta tta caa ttg gca ttg cat ccg gtc gag atg aag gca 48
 Met Gly Lys Leu Leu Gln Leu Ala Leu His Pro Val Glu Met Lys Ala
 1 5 10 15

gct ttg aag ctg aag ttt tgc aga aca ccg cta ttc tcc atc tat gat 96
 Ala Leu Lys Leu Lys Phe Cys Arg Thr Pro Leu Phe Ser Ile Tyr Asp
 20 25 30

cag tcc acg tct cca tat ctc ttg cac tgt ttc gaa ctg ttg aac ttg 144

27

Gln	Ser	Thr	Ser	Pro	Tyr	Leu	Leu	His	Cys	Phe	Glu	Leu	Leu	Asn	Leu		
		35					40					45					
acc	tcc	aga	tcg	ttt	gct	gct	gtg	atc	aga	gag	ctg	cat	cca	gaa	ttg		192
Thr	Ser	Arg	Ser	Phe	Ala	Ala	Val	Ile	Arg	Glu	Leu	His	Pro	Glu	Leu		
		50				55					60						
aga	aac	tgt	gtt	act	ctc	ttt	tat	ttg	att	tta	agg	gct	ttg	gat	acc		240
Arg	Asn	Cys	Val	Thr	Leu	Phe	Tyr	Leu	Ile	Leu	Arg	Ala	Leu	Asp	Thr		
65					70				75					80			
atc	gaa	gac	gat	atg	tcc	atc	gaa	cac	gat	ttg	aaa	att	gac	ttg	ttg		288
Ile	Glu	Asp	Asp	Met	Ser	Ile	Glu	His	Asp	Leu	Lys	Ile	Asp	Leu	Leu		
				85					90					95			
cgt	cac	ttc	cac	gag	aaa	ttg	ttg	tta	act	aaa	tgg	agt	ttc	gac	gga		336
Arg	His	Phe	His	Glu	Lys	Leu	Leu	Thr	Lys	Trp	Ser	Phe	Asp	Gly			
			100					105					110				
aat	gcc	ccc	gat	gtg	aag	gac	aga	gcc	gtt	ttg	aca	gat	ttc	gaa	tcg		384
Asn	Ala	Pro	Asp	Val	Lys	Asp	Arg	Ala	Val	Leu	Thr	Asp	Phe	Glu	Ser		
		115					120					125					
att	ctt	att	gaa	ttc	cac	aaa	ttg	aaa	cca	gaa	tat	caa	gaa	gtc	atc		432
Ile	Leu	Ile	Glu	Phe	His	Lys	Leu	Lys	Pro	Glu	Tyr	Gln	Glu	Val	Ile		
	130					135					140						
aag	gag	atc	acc	gag	aaa	atg	ggg	aat	ggg	atg	gcc	gac	tac	atc	tta		480
Lys	Glu	Ile	Thr	Glu	Lys	Met	Gly	Asn	Gly	Met	Ala	Asp	Tyr	Ile	Leu		
145					150				155					160			
gat	gaa	aat	tac	aac	ttg	aat	ggg	ttg	caa	acc	gtc	cac	gac	tac	gac		528
Asp	Glu	Asn	Tyr	Asn	Leu	Asn	Gly	Leu	Gln	Thr	Val	His	Asp	Tyr	Asp		
				165				170						175			
gtg	tac	tgt	cac	tac	gta	gct	ggg	ttg	gtc	ggg	gat	ggg	ttg	acc	cgt		576
Val	Tyr	Cys	His	Tyr	Val	Ala	Gly	Leu	Val	Gly	Asp	Gly	Leu	Thr	Arg		
			180					185					190				
ttg	att	gtc	att	gcc	aag	ttt	gcc	aac	gaa	tct	ttg	tat	tct	aat	gag		624
Leu	Ile	Val	Ile	Ala	Lys	Phe	Ala	Asn	Glu	Ser	Leu	Tyr	Ser	Asn	Glu		
		195					200					205					
caa	ttg	tat	gaa	agc	atg	ggg	ctt	ttc	cta	caa	aaa	acc	aac	atc	atc		672
Gln	Leu	Tyr	Glu	Ser	Met	Gly	Leu	Phe	Leu	Gln	Lys	Thr	Asn	Ile	Ile		
		210				215					220						
aga	gat	tac	aat	gaa	gat	ttg	gtc	gat	ggg	aga	tcc	ttc	tgg	ccc	aag		720

28

Arg	Asp	Tyr	Asn	Glu	Asp	Leu	Val	Asp	Gly	Arg	Ser	Phe	Trp	Pro	Lys	
225						230				235					240	
gaa	atc	tgg	tca	caa	tac	gct	cct	cag	ttg	aag	gac	ttc	atg	aaa	cct	768
Glu	Ile	Trp	Ser	Gln	Tyr	Ala	Pro	Gln	Leu	Lys	Asp	Phe	Met	Lys	Pro	
				245					250					255		
gaa	aac	gaa	caa	ctg	ggg	ttg	gac	tgt	ata	aac	cac	ctc	gtc	tta	aac	816
Glu	Asn	Glu	Gln	Leu	Gly	Leu	Asp	Cys	Ile	Asn	His	Leu	Val	Leu	Asn	
			260					265					270			
gca	ttg	agt	cat	gtt	atc	gat	gtg	ttg	act	tat	ttg	gcc	ggg	atc	cac	864
Ala	Leu	Ser	His	Val	Ile	Asp	Val	Leu	Thr	Tyr	Leu	Ala	Gly	Ile	His	
			275				280					285				
gag	caa	tcc	act	ttc	caa	ttt	tgt	gcc	att	ccc	caa	gtt	atg	gcc	att	912
Glu	Gln	Ser	Thr	Phe	Gln	Phe	Cys	Ala	Ile	Pro	Gln	Val	Met	Ala	Ile	
			290			295				300						
gca	acc	ttg	gct	ttg	gta	ttc	aac	aac	cgt	gaa	gtg	cta	cat	ggc	aat	960
Ala	Thr	Leu	Ala	Leu	Val	Phe	Asn	Asn	Arg	Glu	Val	Leu	His	Gly	Asn	
305					310				315						320	
gta	aag	att	cgt	aag	ggg	act	acc	tgc	tat	tta	att	ttg	aaa	tca	agg	1008
Val	Lys	Ile	Arg	Lys	Gly	Thr	Thr	Cys	Tyr	Leu	Ile	Leu	Lys	Ser	Arg	
				325				330						335		
act	ttg	cgt	ggc	tgt	gtc	gag	att	ttt	gac	tat	tac	tta	cgt	gat	atc	1056
Thr	Leu	Arg	Gly	Cys	Val	Glu	Ile	Phe	Asp	Tyr	Tyr	Leu	Arg	Asp	Ile	
			340					345					350			
aaa	tct	aaa	ttg	gct	gtg	caa	gat	cca	aat	ttc	tta	aaa	ttg	aac	att	1104
Lys	Ser	Lys	Leu	Ala	Val	Gln	Asp	Pro	Asn	Phe	Leu	Lys	Leu	Asn	Ile	
			355				360					365				
caa	atc	tcc	aag	atc	gaa	cag	ttt	atg	gaa	gaa	atg	tac	cag	gat	aaa	1152
Gln	Ile	Ser	Lys	Ile	Glu	Gln	Phe	Met	Glu	Glu	Met	Tyr	Gln	Asp	Lys	
			370			375					380					
tta	cct	cct	aac	gtg	aag	cca	aat	gaa	act	cca	att	ttc	ttg	aaa	gtt	1200
Leu	Pro	Pro	Asn	Val	Lys	Pro	Asn	Glu	Thr	Pro	Ile	Phe	Leu	Lys	Val	
385					390				395						400	
aaa	gaa	aga	tcc	aga	tac	gat	gat	gaa	ttg	gtt	cca	acc	caa	caa	gaa	1248
Lys	Glu	Arg	Ser	Arg	Tyr	Asp	Asp	Glu	Leu	Val	Pro	Thr	Gln	Gln	Glu	
				405				410					415			
gaa	gag	tac	aag	ttc	aat	atg	gtt	tta	tct	atc	atc	ttg	tcc	gtt	ctt	1296

29

Glu Glu Tyr Lys Phe Asn Met Val Leu Ser Ile Ile Leu Ser Val Leu
 420 425 430

ctt ggg ttt tat tat ata tac act tta cac aga gcg tga
 Leu Gly Phe Tyr Tyr Ile Tyr Thr Leu His Arg Ala
 435 440

1335

<210> 10

<211> 444

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 10

Met Gly Lys Leu Leu Gln Leu Ala Leu His Pro Val Glu Met Lys Ala
 1 5 10 15

Ala Leu Lys Leu Lys Phe Cys Arg Thr Pro Leu Phe Ser Ile Tyr Asp
 20 25 30

Gln Ser Thr Ser Pro Tyr Leu Leu His Cys Phe Glu Leu Leu Asn Leu
 35 40 45

Thr Ser Arg Ser Phe Ala Ala Val Ile Arg Glu Leu His Pro Glu Leu
 50 55 60

Arg Asn Cys Val Thr Leu Phe Tyr Leu Ile Leu Arg Ala Leu Asp Thr
 65 70 75 80

Ile Glu Asp Asp Met Ser Ile Glu His Asp Leu Lys Ile Asp Leu Leu
 85 90 95

Arg His Phe His Glu Lys Leu Leu Leu Thr Lys Trp Ser Phe Asp Gly
 100 105 110

30

Asn Ala Pro Asp Val Lys Asp Arg Ala Val Leu Thr Asp Phe Glu Ser
115 120 125

Ile Leu Ile Glu Phe His Lys Leu Lys Pro Glu Tyr Gln Glu Val Ile
130 135 140

Lys Glu Ile Thr Glu Lys Met Gly Asn Gly Met Ala Asp Tyr Ile Leu
145 150 155 160

Asp Glu Asn Tyr Asn Leu Asn Gly Leu Gln Thr Val His Asp Tyr Asp
165 170 175

Val Tyr Cys His Tyr Val Ala Gly Leu Val Gly Asp Gly Leu Thr Arg
180 185 190

Leu Ile Val Ile Ala Lys Phe Ala Asn Glu Ser Leu Tyr Ser Asn Glu
195 200 205

Gln Leu Tyr Glu Ser Met Gly Leu Phe Leu Gln Lys Thr Asn Ile Ile
210 215 220

Arg Asp Tyr Asn Glu Asp Leu Val Asp Gly Arg Ser Phe Trp Pro Lys
225 230 235 240

Glu Ile Trp Ser Gln Tyr Ala Pro Gln Leu Lys Asp Phe Met Lys Pro
245 250 255

Glu Asn Glu Gln Leu Gly Leu Asp Cys Ile Asn His Leu Val Leu Asn
260 265 270

Ala Leu Ser His Val Ile Asp Val Leu Thr Tyr Leu Ala Gly Ile His
275 280 285

Glu Gln Ser Thr Phe Gln Phe Cys Ala Ile Pro Gln Val Met Ala Ile
290 295 300

31

Ala Thr Leu Ala Leu Val Phe Asn Asn Arg Glu Val Leu His Gly Asn
305 310 315 320

Val Lys Ile Arg Lys Gly Thr Thr Cys Tyr Leu Ile Leu Lys Ser Arg
325 330 335

Thr Leu Arg Gly Cys Val Glu Ile Phe Asp Tyr Tyr Leu Arg Asp Ile
340 345 350

Lys Ser Lys Leu Ala Val Gln Asp Pro Asn Phe Leu Lys Leu Asn Ile
355 360 365

Gln Ile Ser Lys Ile Glu Gln Phe Met Glu Glu Met Tyr Gln Asp Lys
370 375 380

Leu Pro Pro Asn Val Lys Pro Asn Glu Thr Pro Ile Phe Leu Lys Val
385 390 395 400

Lys Glu Arg Ser Arg Tyr Asp Asp Glu Leu Val Pro Thr Gln Gln Glu
405 410 415

Glu Glu Tyr Lys Phe Asn Met Val Leu Ser Ile Ile Leu Ser Val Leu
420 425 430

Leu Gly Phe Tyr Tyr Ile Tyr Thr Leu His Arg Ala
435 440

<210> 11

<211> 35

<212> DNA

<213> artificial sequence

<220>

<221> Primer

<222> (1)..(35)

<223> AtHT-5'

<400> 11

ctgcggccgc atcatggacc aattggtgaa aactg

35

<210> 12

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<221> Primer

<222> (1)..(32)

<223> AtHT-3'

<400> 12

aactcgagag acacatggtg ctgttggtgct tc

32

<210> 13

<211> 60

<212> DNA

<213> Artificial sequence

<220>

<221> Primer

<222> (1)..(60)

<223> ERG5-Crelox-5'

<400> 13

atgagttctg tcgcagaaaa tataatacaa catgccactc ccagctgaag cttcgtacgc 60

<210> 14

<211> 62

<212> DNA

<213> Artificial sequence

<220>

<221> Primer

<222> (1)..(62)

<223> ERG5-Crelox-3'

<400> 14

ttattcgaag acttctccag taattgggtc tctctttttg gcataggcca ctagtggatc 60

tg 62